SEQUENCE LISTING

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<120> NOVEL PROTEIN PHOSPHATASES AND DIAGNOSIS AND TREATMENT OF PHOSPHATASE-RELATED DISORDERS

<130> 034536-0726

<140> 10/049,515
<141> 2002-06-14

<150> PCT/US00/22158
<151> 2000-08-11

<160> 45

<170> PatentIn Ver. 3.2

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Asp Gln Gly Val Arg His Leu Val Ser Leu Thr Glu Arg Gly Pro Pro
35 40 45

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His Ser Asp Ser Cys Pro Gly Leu Thr Leu His Arg Met Arg Ile Pro
     50                  55                  60

Asp Phe Cys Pro Pro Ser Pro Glu Gln Ile Asp Gln Phe Val Lys Ile
 65                  70                  75                  80

Val Asp Glu Ala Asn Ala Arg Gly Glu Ala Val Gly Val His Cys Ala
                 85                  90                  95

Leu Gly Phe Gly Arg Thr Gly Thr Met Leu Ala Cys Tyr Leu Val Lys
            100                 105                 110

Glu Arg Ala Leu Ala Ala Gly Asp Ala Ile Ala Glu Ile Arg Arg Leu
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Arg Pro Gly Ser Ile Glu Thr Tyr Glu Gln Glu Lys Ala Val Phe Gln
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Phe Tyr Gln Arg Thr Lys
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Val Arg Ala Gly Ile Thr Leu Cys Val Asn Val Ser Arg Gln Gln Pro
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Gly Pro Arg Ala Pro Gly Val Ala Glu Leu Arg Val Pro Val Phe Asp
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Asp Pro Ala Glu Asp Leu Leu Thr His Leu Glu Pro Thr Cys Ala Ala
65                  70                  75                  80

Met Glu Ala Ala Val Arg Asp Gly Gly Ser Cys Leu Val Tyr Cys Lys
                85                  90                  95

Asn Gly Arg Ser Arg Ser Ala Ala Val Cys Thr Ala Tyr Leu Met Arg
            100                 105                 110

His Arg Gly His Ser Leu Asp Arg Ala Phe Gln Met Val Lys Ser Ala
        115                 120                 125

Arg Pro Val Ala Glu Pro Asn Leu Gly Phe Trp Ala Gln Leu Gln Lys
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<400> 6

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             20                  25                  30

His Ile Leu Ser Val His Asp Thr Ala Arg Pro Met Leu Glu Gly Val
         35                  40                  45

Lys Tyr Leu Cys Ile Pro Ala Ala Asp Thr Pro Ser Gln Asn Leu Thr
     50                  55                  60

Arg His Phe Lys Glu Ser Ile Lys Phe Ile His Glu Cys Arg Leu Gln
 65                  70                  75                  80

Gly Glu Ser Cys Leu Val His Cys Leu Ala Gly Val Ser Arg Ser Val
                 85                  90                  95

Thr Leu Val Ile Ala Tyr Ile Met Thr Val Thr Asp Phe Gly Trp Glu
            100                 105                 110

Asp Ala Leu His Thr Val Arg Ala Gly Arg Ser Cys Ala Asn Pro Asn
        115                 120                 125

Leu Gly Phe Gln Arg Gln Leu Gln Glu Phe Glu Lys His Glu Val His
    130                 135                 140

Gln Tyr Arg Gln Trp Leu Arg Glu Glu Tyr Gly Glu Asn Pro Leu Arg
145                 150                 155                 160

Asp Ala Glu Glu Ala Lys Asn Ile Leu Ala Ala Pro Gly Ile Leu Lys
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Tyr Trp Ala Phe Leu Arg Arg Leu
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Arg Leu Leu Trp Val Arg Arg Thr Ala Thr Leu Thr His Ile Asn Glu
35 40 45

Val Trp Pro Asn Leu Phe Leu Gly Asp Ala Tyr Ala Ala Arg Asp Lys
50 55 60

Gly Arg Leu Ile Gln Leu Gly Ile Thr His Val Val Asn Val Ala Ala
65 70 75 80

Gly Lys Phe Gln Val Asp Thr Gly Ala Lys Phe Tyr Arg Gly Thr Pro
85 90 95

Leu Glu Tyr Tyr Gly Ile Glu Ala Asp Asp Asn Pro Phe Phe Asp Leu
100 105 110

Ser Val His Phe Leu Pro Val Ala Arg Tyr Ile Arg Asp Ala Leu Asn
115 120 125

Ile Pro Arg Ser Arg Val Leu Val His Cys Ala Met Gly Val Ser Arg
130 135 140

Ser Ala Thr Ile Val Leu Ala Phe Leu Met Ile Phe Glu Asn Met Thr
145 150 155 160

Leu Val Asp Ala Ile Gln Thr Val Gln Ala His Arg Asp Ile Cys Pro
165 170 175

Asn Ser Gly Phe Leu Arg Gln Leu Gln Val Leu Asp Asn Arg Leu Arg
180 185 190

Arg Glu Thr Gly Arg Leu
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Glu Thr Trp Glu Asp Ala Thr Val His Val Val Glu Thr Glu Pro Ser
         35                  40                  45

Gly Gly Gly Gly Cys Gly Tyr Val Gln Asp Leu Thr Leu Asp Leu Gln
     50                  55                  60

Val Gly Val Ile Lys Pro Trp Leu Leu Leu Gly Ser Gln Asp Ala Ala
 65                  70                  75                  80

His Asp Leu Glu Leu Leu Arg Lys His Lys Val Thr His Ile Leu Asn
                 85                  90                  95

Val Ala Tyr Gly Val Glu Asn Ala Phe Leu Ser Glu Phe Thr Tyr Lys
            100                 105                 110

Thr Ile Ser Ile Leu Asp Val Pro Glu Thr Asn Ile Leu Ser Tyr Phe
        115                 120                 125

Pro Glu Cys Phe Glu Phe Ile Glu Gln Ala Lys Leu Lys Asp Gly Val
    130                 135                 140

Val Leu Val His Cys Asn Ala Gly Val Ser Arg Ala Ala Ala Ile Val
145                 150                 155                 160

Ile Gly Phe Leu Met Ser Ser Glu Glu Ala Thr Phe Thr Thr Ala Leu
                165                 170                 175

Ser Leu Val Lys Glu Ala Arg Pro Ser Ile Cys Pro Asn Pro Gly Phe
            180                 185                 190

Met Glu Gln Leu Arg Thr Tyr Gln Val Gly Lys Glu Ser Asn Gly Gly
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<213> Homo sapiens

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20 25 30

His Ile Leu Ser Val His Asp Ser Ala Arg Pro Met Leu Glu Gly Val
35 40 45

Lys Tyr Leu Cys Ile Pro Ala Ala Asp Ser Pro Ser Gln Asn Leu Thr
50 55 60

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Arg His Phe Lys Glu Ser Ile Lys Phe Ile His Glu Cys Arg Leu Arg
 65                  70                  75                  80

Gly Glu Ser Cys Leu Val His Cys Leu Ala Gly Val Ser Arg Ser Val
                85                  90                  95

Thr Leu Val Ile Ala Tyr Ile Met Thr Val Thr Asp Phe Gly Trp Glu
            100                 105                 110

Asp Ala Leu His Thr Val Arg Ala Gly Arg Ser Cys Ala Asn Pro Asn
        115                 120                 125

Val Gly Phe Gln Arg Gln Leu Gln Glu Phe Glu Lys His Glu Val His
    130                 135                 140

Gln Tyr Arg Gln Trp Leu Lys Glu Glu Tyr Gly Glu Ser Pro Leu Gln
145                 150                 155                 160

Asp Ala Glu Glu Ala Lys Asn Ile Leu Ala Ala Pro Gly Ile Leu Lys
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             20                  25                  30

Gly Gly Gly Ala Ser Ala Ala Ser Ser Met Leu Pro Gln Ser Val Pro
         35                  40                  45

Thr Thr Pro Asp Ile Glu Asn Ala Glu Leu Thr Pro Ile Leu Pro Phe
     50                  55                  60

Leu Phe Leu Gly Asn Glu Gln Asp Ala Gln Asp Leu Asp Thr Met Gln
 65                  70                  75                  80

Arg Leu Asn Ile Gly Tyr Val Ile Asn Val Thr Thr His Leu Pro Leu
                 85                  90                  95

Tyr His Tyr Glu Lys Gly Leu Phe Asn Tyr Lys Arg Leu Pro Ala Thr
            100                 105                 110

Asp Ser Asn Lys Gln Asn Leu Arg Gln Tyr Phe Glu Glu Ala Phe Glu
        115                 120                 125

Phe Ile Glu Glu Ala His Gln Cys Gly Lys Gly Leu Leu Ile His Cys
    130                 135                 140

Gln Ala Gly Val Ser Arg Ser Ala Thr Ile Val Ile Ala Tyr Leu Met
145                 150                 155                 160

Lys His Thr Arg Met Thr Met Thr Asp Ala Tyr Lys Phe Val Lys Gly
                165                 170                 175

Lys Arg Pro Ile Ile Ser Pro Asn Leu Asn Phe Met Gly Gln Leu Leu
            180                 185                 190

Glu Phe Glu Asp Asp Leu Asn Asn Gly Val Thr Pro Arg Ile Leu Thr
        195                 200                 205

Pro Lys Leu Met Gly Met Glu Thr Val Val
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<210> 16
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<213> Mus sp.

<400> 16

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            20                  25                  30

Gly Leu Tyr Leu Gly Gly Ala Ala Ala Val Ala Glu Pro Gly His Leu
        35                  40                  45

Arg Glu Ala Gly Ile Thr Ala Val Leu Thr Val Asp Ser Glu Pro Ala
    50                  55                  60

Phe Pro Ala Gly Ala Gly Phe Glu Gly Leu Arg Ser Leu Phe Val Pro
65                  70                  75                  80

Ala Leu Asp Lys Pro Glu Thr Asp Leu Leu Ser His Leu Asp Arg Cys
                85                  90                  95

Val Ala Phe Ile Gly Gln Ala Arg Ser Glu Gly Arg Ala Val Leu Val
            100                 105                 110

His Cys His Ala Gly Val Ser Arg Ser Val Ala Val Val Met Ala Phe
        115                 120                 125

Ile Met Lys Thr Asp Gln Leu Thr Phe Glu Lys Ala Tyr Asp Ile Leu
    130                 135                 140

Arg Thr Val Lys Pro Glu Ala Lys Val Asn Glu Gly Phe Glu Trp Gln
145                 150                 155                 160

Leu Lys Leu Tyr Glu Ala Met Gly Tyr Glu Val Asp Thr Ser Ser Ala
                165                 170                 175

Phe Tyr Lys Gln Tyr Arg Leu Gln Lys Val Thr Glu Lys Tyr Pro Glu
            180                 185                 190

Leu Trp Asn Leu Pro Gln Glu Leu Phe Ala Val Asp Pro Thr Thr Ile
        195                 200                 205
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Ser Gln Gly Leu Lys Asp Asp Ile Leu Tyr Lys Cys Arg Lys Cys Arg
    210                 215                 220

Arg Ser Leu Phe Arg His Ser Ser Ile Leu Gly His Ser Glu Gly Ser
225                 230                 235                 240

Gly Pro Ile Ala Phe Ala His Lys Arg Thr Ala Pro Ser Ser Val Leu
                245                 250                 255

Thr Thr Gly Ser Gln Ala Gln Cys Thr Ser Tyr Phe Ile Glu Pro Val
            260                 265                 270

Gln Trp Met Glu Ser Thr Leu Leu Gly Val Met Asp Gly Gln Leu Leu
        275                 280                 285

Cys Pro Lys Cys Ser Ala Lys Leu Gly Ser Phe Asn Trp Tyr Gly Glu
    290                 295                 300

Gln Cys Ser Cys Gly Arg Trp Ile Thr Pro Ala Phe Gln Ile His Lys
305                 310                 315                 320

Asn Arg Val Asp Glu Met Lys Met Leu Pro Ala Leu Gly Ser Gln Thr
                325                 330                 335

Lys Lys Leu
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<210> 17
<211> 904
<212> DNA
<213> Homo sapiens

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agtccaggca tctccctacc agccgcccac attggcttcg ctgcagcgct tgctgtgggt 180
ccgtcaggct gccacactga accatatcga tgaggtctgg cccagcctct tcctgggaga 240
tgcgtacgca gcccgggaca agagcaagct gatccagctg ggaatcaccc acgttgtgaa 300
tgccgctgca ggcaagttcc aggtggacac aggtgccaaa ttctaccgtg gaatgtccct 360
ggagtactat ggcattgagg cggacgacaa ccccttcttc gacctcagtg tctactttct 420
gcctgttgct cgatacatcc gagctgccct cagtgttccc caaggccgcg tgctggtaca 480
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ctcaggcttc ctccggcagc tccaggttct ggacaaccga ctggggcggg agacggggcg 660
gttctgatct ggcaggcagc caggatccct gacccttggc ccaaccccac cagcctggcc 720
ctgggaacag caggctctgc tgtttctagt gaccctgaga tgtaaacagc aagtgggggc 780
tgaggcagag gcagggatag ctgggtggtg acctcttagc gggtggattt ccctgaccca 840
attcagagat tctttatgca aaagtgagtt cagtccatct ctataataaa atattcatcg 900
tcat 904

<210> 18
<211> 198
<212> PRT
<213> Homo sapiens

<400> 18
Met Asp Ser Leu Gln Lys Gln Asp Leu Arg Arg Pro Lys Ile His Gly
1 5 10 15

Ala Val Gln Ala Ser Pro Tyr Gln Pro Pro Thr Leu Ala Ser Leu Gln
20 25 30

Arg Leu Leu Trp Val Arg Gln Ala Ala Thr Leu Asn His Ile Asp Glu
35 40 45

Val Trp Pro Ser Leu Phe Leu Gly Asp Ala Tyr Ala Ala Arg Asp Lys
50 55 60

Ser Lys Leu Ile Gln Leu Gly Ile Thr His Val Val Asn Ala Ala Ala
65 70 75 80

Gly Lys Phe Gln Val Asp Thr Gly Ala Lys Phe Tyr Arg Gly Met Ser
85 90 95

Leu Glu Tyr Tyr Gly Ile Glu Ala Asp Asp Asn Pro Phe Phe Asp Leu
100 105 110

Ser Val Tyr Phe Leu Pro Val Ala Arg Tyr Ile Arg Ala Ala Leu Ser
115 120 125

Val Pro Gln Gly Arg Val Leu Val His Cys Ala Met Gly Val Ser Arg
130 135 140

Ser Ala Thr Leu Val Leu Ala Phe Leu Met Ile Tyr Glu Asn Met Thr
145 150 155 160

Leu Val Glu Ala Ile Gln Thr Val Gln Ala His Arg Asn Ile Cys Pro
165 170 175

Asn Ser Gly Phe Leu Arg Gln Leu Gln Val Leu Asp Asn Arg Leu Gly
180 185 190

Arg Glu Thr Gly Arg Phe
195

<210> 19
<211> 908
<212> DNA
<213> Homo sapiens

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ccagcgtaga gagacctcgg accagccgcc ttgatgacag catccgcgtc ctccttttca 180
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tttctcagca atggtgtggc cgccaacgac aaactccttc tgtccagcaa tcgcatcacc 300
gccattgtca atgcctcggt ggaagtggtc aacgtattct tcgagggcat tcagtacata 360
aaggtgcctg ttaccgatgc tcgtgactcg cgtctctacg acttttttga ccccattgct 420
gatcttatcc acaccatcga tatgaggcag ggccgtacgc tgctgcactg catggctgga 480
gtgagccgtt ccgcctcact gtgccttgcg tacctcatga ataccactc catgtcgctg 540
ctggacgccc atacatggac caagtcgcgc cgccccatca tccggcccaa caacggcttt 600
tgggaacagc tcatcaatta cgaattcaag ctgtttaata acaacaccgt gcgcatgatc 660

aactcgccgg taggtaacat ccctgacatc tatgagaagg acctacgtat gatgatatca 720
atgtaagcca tcccggccag cccctgacat ctgccatcga tcttgcacca agactgaact 780
ttgaacactg acattttgtt agtaaagaaa accggatggt gccttgttaa agggcaagaa 840
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tgaaacat 908

<210> 20
<211> 190
<212> PRT
<213> Homo sapiens

<400> 20
Met Thr Ala Ser Ala Ser Ser Phe Ser Ser Ser Gln Gly Val Gln Gln
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Pro Ser Ile Tyr Ser Phe Ser Gln Ile Thr Arg Ser Leu Phe Leu Ser
20 25 30

Asn Gly Val Ala Ala Asn Asp Lys Leu Leu Leu Ser Ser Asn Arg Ile
35 40 45

Thr Ala Ile Val Asn Ala Ser Val Glu Val Val Asn Val Phe Phe Glu
50 55 60

Gly Ile Gln Tyr Ile Lys Val Pro Val Thr Asp Ala Arg Asp Ser Arg
65 70 75 80

Leu Tyr Asp Phe Phe Asp Pro Ile Ala Asp Leu Ile His Thr Ile Asp
85 90 95

Met Arg Gln Gly Arg Thr Leu Leu His Cys Met Ala Gly Val Ser Arg
100 105 110

Ser Ala Ser Leu Cys Leu Ala Tyr Leu Met Lys Tyr His Ser Met Ser
115 120 125

Leu Leu Asp Ala His Thr Trp Thr Lys Ser Arg Arg Pro Ile Ile Arg
130 135 140

Pro Asn Asn Gly Phe Trp Glu Gln Leu Ile Asn Tyr Glu Phe Lys Leu
145 150 155 160

Phe Asn Asn Asn Thr Val Arg Met Ile Asn Ser Pro Val Gly Asn Ile
165 170 175

Pro Asp Ile Tyr Glu Lys Asp Leu Arg Met Met Ile Ser Met
180 185 190

<210> 21
<211> 775
<212> DNA
<213> Homo sapiens

<400> 21
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cctcgtgtgc cttcccagtt cagttccggc agccctcagt cagcggcctc tcgcagataa 180
ccaaaagcct gtatatcagc aatggtgtgg ccgccaacaa caagctcatg ctgtctagca 240
accagatcac catggtcatc aatgtctcag tggaggtagt gaacaccttg tatgaggata 300
tccagtacat gcaggtacct gtggctgact ccctaactc acgtctctgt gacttctttg 360
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tgcacatggt cagttcccca gtgggaatga tccctgacat ctatgagaag gaagtccgtt 660
tgatgattcc actgtgagcc atcccacgag cccctgcatt ggagtcagag gtacagatct 720
attgttgatc ttacaccaag atccaaactt gaacattcta cttttgttga tacag 775

<210> 22
<211> 188
<212> PRT
<213> Homo sapiens

<400> 22
Met Thr Ala Pro Ser Cys Ala Phe Pro Val Gln Phe Arg Gln Pro Ser
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Val Ser Gly Leu Ser Gln Ile Thr Lys Ser Leu Tyr Ile Ser Asn Gly
20 25 30

Val Ala Ala Asn Asn Lys Leu Met Leu Ser Ser Asn Gln Ile Thr Met
35 40 45

Val Ile Asn Val Ser Val Glu Val Val Asn Thr Leu Tyr Glu Asp Ile
50 55 60

Gln Tyr Met Gln Val Pro Val Ala Asp Ser Pro Asn Ser Arg Leu Cys
65 70 75 80

Asp Phe Phe Asp Pro Ile Ala Asp His Ile His Ser Val Glu Met Lys
85 90 95

Gln Gly Arg Thr Leu Leu His Cys Ala Ala Gly Val Ser Arg Ser Ala
100 105 110

Ala Leu Cys Leu Ala Tyr Leu Met Lys Tyr His Ala Met Ser Leu Leu
115 120 125

Asp Ala His Thr Trp Thr Lys Ser Cys Arg Pro Ile Ile Arg Pro Asn
130 135 140

Ser Gly Phe Trp Glu Gln Leu Ile His Tyr Glu Phe Gln Leu Phe Gly
145 150 155 160

Lys Asn Thr Val His Met Val Ser Ser Pro Val Gly Met Ile Pro Asp
165 170 175

Ile Tyr Glu Lys Glu Val Arg Leu Met Ile Pro Leu
180 185

<210> 23
<211> 1251
<212> DNA
<213> Homo sapiens

<400> 23
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taacagtgga ctcggaggag cccagcttca aggcggggcc tggggtcgag gatctatggc 240
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cctttgaaaa agcctatgaa aagctccaga ttctcaaacc agaggctaag atgaatgagg 480
ggtttgagtg gcaactgaaa ttataccagg caatgggata tgaagtggat acctctagtg 540
caatttataa gcaatatcgt ttacaaaagg ttacagagaa gtatccagaa ttgcagaatt 600
tacctcaaga actctttgct gttgacccaa ctaccgtttc acaaggattg aaagatgagg 660
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<210> 24
<211> 340
<212> PRT
<213> Homo sapiens

<400> 24
Met Leu Glu Ala Pro Gly Pro Ser Asp Gly Cys Glu Leu Ser Asn Pro
1 5 10 15

Ser Ala Ser Arg Val Ser Cys Ala Gly Gln Met Leu Glu Val Gln Pro
20 25 30

Gly Leu Tyr Phe Gly Gly Ala Ala Ala Val Ala Glu Pro Asp His Leu
35 40 45

Arg Glu Ala Gly Ile Thr Ala Val Leu Thr Val Asp Ser Glu Glu Pro
50 55 60

Ser Phe Lys Ala Gly Pro Gly Val Glu Asp Leu Trp Arg Leu Phe Val
65 70 75 80

Pro Ala Leu Asp Lys Pro Glu Thr Asp Leu Leu Ser His Leu Asp Arg
85 90 95

Cys Val Ala Phe Ile Gly Gln Ala Arg Ala Glu Gly Arg Ala Val Leu
100 105 110

Val His Cys His Ala Gly Val Ser Arg Ser Val Ala Ile Ile Thr Ala
115 120 125

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Phe Leu Met Lys Thr Asp Gln Leu Pro Phe Glu Lys Ala Tyr Glu Lys
    130                 135                 140

Leu Gln Ile Leu Lys Pro Glu Ala Lys Met Asn Glu Gly Phe Glu Trp
145                 150                 155                 160

Gln Leu Lys Leu Tyr Gln Ala Met Gly Tyr Glu Val Asp Thr Ser Ser
                165                 170                 175

Ala Ile Tyr Lys Gln Tyr Arg Leu Gln Lys Val Thr Glu Lys Tyr Pro
            180                 185                 190

Glu Leu Gln Asn Leu Pro Gln Glu Leu Phe Ala Val Asp Pro Thr Thr
        195                 200                 205

Val Ser Gln Gly Leu Lys Asp Glu Val Leu Tyr Lys Cys Arg Lys Cys
    210                 215                 220

Arg Arg Ser Leu Phe Arg Ser Ser Ser Ile Leu Asp His Arg Glu Gly
225                 230                 235                 240

Ser Gly Pro Ile Ala Phe Ala His Lys Arg Met Thr Pro Ser Ser Met
                245                 250                 255

Leu Thr Thr Gly Arg Gln Ala Gln Cys Thr Ser Tyr Phe Ile Glu Pro
            260                 265                 270

Val Gln Trp Met Glu Ser Ala Leu Leu Gly Val Met Asp Gly Gln Leu
        275                 280                 285

Leu Cys Pro Lys Cys Ser Ala Lys Leu Gly Ser Phe Asn Trp Tyr Gly
    290                 295                 300

Glu Gln Cys Ser Cys Gly Arg Trp Ile Thr Pro Ala Phe Gln Ile His
305                 310                 315                 320

Lys Asn Arg Val Asp Glu Met Lys Ile Leu Pro Val Leu Gly Ser Gln
                325                 330                 335

Thr Gly Lys Ile
            340
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<210> 25
<211> 687
<212> DNA
<213> Homo sapiens

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gcacctggag cccacgtgcg ccgccatgga ggccgcggtg cgcgccggcg gcgcctgcct 360
agtctactgc aagaacggcc gcagccagct cggcgccgtc tgcaccgcgt acctcatgcg 420
gcaccgcggc ctcagcctgg cgaaggcctt ccagatggtg aagagcgctc gcccggtagc 480

agaaccgaac ccgggcttct ggtctcagct ccagaagtat gaggaggccc tccaggccca 540
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cttcctcact gtcatatcga gttttcc 687

<210> 26
<211> 176
<212> PRT
<213> Homo sapiens

<400> 26
Met Gly Pro Ser Glu Ala Gly Arg Arg Gly Ala Ala Ser Pro Val Pro
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Pro Pro Leu Val Arg Val Ala Pro Ser Leu Phe Leu Gly Ser Ala Arg
20 25 30

Ala Ala Gly Ala Glu Glu Gln Leu Ala Arg Ala Gly Val Thr Leu Cys
35 40 45

Val Asn Val Ser Arg Gln Gln Pro Gly Pro Arg Ala Pro Gly Val Ala
50 55 60

Glu Leu Arg Val Pro Val Phe Asp Asp Pro Ala Glu Asp Leu Leu Ala
65 70 75 80

His Leu Glu Pro Thr Cys Ala Ala Met Glu Ala Ala Val Arg Ala Gly
85 90 95

Gly Ala Cys Leu Val Tyr Cys Lys Asn Gly Arg Ser Gln Leu Gly Ala
100 105 110

Val Cys Thr Ala Tyr Leu Met Arg His Arg Gly Leu Ser Leu Ala Lys
115 120 125

Ala Phe Gln Met Val Lys Ser Ala Arg Pro Val Ala Glu Pro Asn Pro
130 135 140

Gly Phe Trp Ser Gln Leu Gln Lys Tyr Glu Glu Ala Leu Gln Ala Gln
145 150 155 160

Ser Cys Leu Gln Gly Glu Pro Pro Ala Leu Gly Leu Gly Pro Glu Ala
165 170 175

<210> 27
<211> 901
<212> DNA
<213> Homo sapiens

<400> 27
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ccggaataat ctcaggaagc aatgcaccag ggtgacaacg ctaactggaa agaaaattat 180
agaaacatgg aaagatgcca gaattcatgt tgtggaagaa gtagagccga gcagtggggg 240
tggttgtggt tatgtgcagg accttagctc ggacctgcaa gttggcgtta ttaagccatg 300
gttgctccta gggtcacaag atgctgctca tgatttggat acactgaaaa agaataaggt 360

gactcatatt cttaatgttg catatggagt tgaaaatgct ttcctcagtg actttacata 420
taagagcatt tctatattgg atctgcctga aaccaacatc ctgtcttatt ttccagaatg 480
ttttgaattt attgaagaag caaaaagaaa agatggagtg gttcttgttc attgtaatgc 540
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tgacttctat agccatcttt tccctttttt ggagagtaga ctagcaaaat tccctttttt 840
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g 901

<210> 28
<211> 217
<212> PRT
<213> Homo sapiens

<400> 28

Met	Tyr	Ser	Leu	Asn	Gln	Glu	Ile	Lys	Ala	Phe	Ser	Arg	Asn	Asn	Leu
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			20					25					30		
Glu	Thr	Trp	Lys	Asp	Ala	Arg	Ile	His	Val	Val	Glu	Glu	Val	Glu	Pro
		35					40					45			
Ser	Ser	Gly	Gly	Gly	Cys	Gly	Tyr	Val	Gln	Asp	Leu	Ser	Ser	Asp	Leu
	50					55					60				
Gln	Val	Gly	Val	Ile	Lys	Pro	Trp	Leu	Leu	Leu	Gly	Ser	Gln	Asp	Ala
65					70					75					80
Ala	His	Asp	Leu	Asp	Thr	Leu	Lys	Lys	Asn	Lys	Val	Thr	His	Ile	Leu
				85					90					95	
Asn	Val	Ala	Tyr	Gly	Val	Glu	Asn	Ala	Phe	Leu	Ser	Asp	Phe	Thr	Tyr
			100					105					110		
Lys	Ser	Ile	Ser	Ile	Leu	Asp	Leu	Pro	Glu	Thr	Asn	Ile	Leu	Ser	Tyr
		115					120					125			
Phe	Pro	Glu	Cys	Phe	Glu	Phe	Ile	Glu	Glu	Ala	Lys	Arg	Lys	Asp	Gly
	130					135					140				
Val	Val	Leu	Val	His	Cys	Asn	Ala	Gly	Val	Ser	Arg	Ala	Ala	Ala	Ile
145					150					155					160
Val	Ile	Gly	Phe	Leu	Met	Asn	Ser	Glu	Gln	Thr	Ser	Phe	Thr	Ser	Ala
				165					170					175	
Phe	Ser	Leu	Val	Lys	Asn	Ala	Arg	Pro	Ser	Ile	Cys	Pro	Asn	Ser	Gly
			180					185					190		
Phe	Met	Glu	Gln	Leu	Arg	Thr	Tyr	Gln	Glu	Gly	Lys	Glu	Ser	Asn	Lys
		195					200					205			

Cys Asp Arg Ile Gln Glu Asn Ser Ser
210 215

<210> 29
<211> 2050
<212> DNA
<213> Homo sapiens

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<223> a, c, g, t, other or unknown

<220>
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<222> (2010)
<223> a, c, g, t, other or unknown

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<221> modified_base
<222> (2032)
<223> a, c, g, t, other or unknown

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tctaagtcca tcaagtgggg tgggcagccc tgtgtcaggg acccccaagc agctagccag 720
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cattaaaaat ttaatacaac ttggtttctn ccccttttttc ctttaaagct antttgtaaa 2040
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<210> 30
<211> 482
<212> PRT
<213> Homo sapiens

<400> 30
Met Pro Pro Ser Pro Leu Asp Asp Arg Val Val Val Ala Leu Ser Arg
1 5 10 15

Pro Val Arg Pro Gln Asp Leu Asn Leu Cys Leu Asp Ser Ser Tyr Leu
20 25 30

Gly Ser Ala Asn Pro Gly Ser Asn Ser His Pro Pro Val Ile Ala Thr
35 40 45

Thr Val Val Ser Leu Lys Ala Ala Asn Leu Thr Tyr Met Pro Ser Ser
50 55 60

Ser Gly Ser Ala Arg Ser Leu Asn Cys Gly Cys Ser Ser Ala Ser Cys
65 70 75 80

Cys Thr Val Ala Thr Tyr Asp Lys Asp Asn Gln Ala Gln Thr Gln Ala
85 90 95

Ile Ala Ala Gly Thr Thr Thr Thr Ala Ile Gly Thr Ser Thr Thr Cys
100 105 110

Pro Ala Asn Gln Met Val Asn Asn Asn Glu Asn Thr Gly Ser Leu Ser
115 120 125

Pro Ser Ser Gly Val Gly Ser Pro Val Ser Gly Thr Pro Lys Gln Leu
130 135 140

Ala Ser Ile Lys Ile Ile Tyr Pro Asn Asp Leu Ala Lys Lys Met Thr
145 150 155 160

Lys Cys Ser Lys Ser His Leu Pro Ser Gln Gly Pro Val Ile Ile Asp
165 170 175

Cys Arg Pro Phe Met Glu Tyr Asn Lys Ser His Ile Gln Gly Ala Val
180 185 190

His Ile Asn Cys Ala Asp Lys Ile Ser Arg Arg Arg Leu Gln Gln Gly
195 200 205

Lys Ile Thr Val Leu Asp Leu Ile Ser Cys Arg Glu Gly Lys Asp Ser
210 215 220

Phe Lys Arg Ile Phe Ser Lys Glu Ile Ile Val Tyr Asp Glu Asn Thr
225 230 235 240

Asn Glu Pro Ser Arg Val Met Pro Ser Gln Pro Leu His Ile Val Leu
245 250 255

Glu Ser Leu Lys Arg Glu Gly Lys Glu Pro Leu Val Leu Lys Gly Gly
260 265 270

Leu Ser Ser Phe Lys Gln Asn His Glu Asn Leu Cys Asp Asn Ser Leu
275 280 285

Gln Leu Gln Glu Cys Arg Glu Val Gly Gly Gly Ala Ser Gly Ala Ser
290 295 300

Ser Leu Leu Pro Gln Pro Ile Pro Thr Thr Pro Asp Ile Glu Asn Ala
305 310 315 320

Glu Leu Thr Pro Ile Leu Pro Phe Leu Phe Leu Gly Asn Glu Gln Asp
325 330 335

Val Arg Asp Leu Asp Thr Met Gln Arg Leu Asn Ile Gly Tyr Val Ile
340 345 350

Asn Val Thr Thr His Leu Pro Leu Tyr His Tyr Glu Lys Gly Leu Phe
355 360 365

Asn Tyr Lys Arg Leu Pro Ser Thr Asp Ser Asn Lys Gln Asn Leu Arg
370 375 380

Gln Tyr Phe Glu Glu Ala Phe Glu Phe Ile Glu Glu Ala His Gln Cys
385 390 395 400

Gly Lys Gly Leu Leu Ile His Cys Gln Ala Gly Val Ser Arg Ser Ala
405 410 415

Thr Ile Val Ile Ala Tyr Leu Met Lys His Thr Arg Met Thr Met Thr
420 425 430

Asp Ala Tyr Lys Phe Val Lys Gly Lys Arg Pro Ile Ile Ser Pro Asn
435 440 445

Leu Asn Phe Met Gly Gln Leu Leu Glu Phe Glu Glu Asp Leu Asn Asn
450 455 460

Gly Val Thr Pro Arg Ile Leu Thr Pro Lys Leu Met Gly Val Glu Thr
465 470 475 480

Val Val

<210> 31
<211> 1026
<212> DNA
<213> Homo sapiens

<400> 31
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gccctgcgcc acgtgcagga gctccggccc atcgcccgcc ccaaccctgg cttcctgcgc 420

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caggcagccc cgaaagaaga gcctgggcca cggccacgta taaacctccg aggggtcatg 660
aggtccatca gtcttctgga gccctccttg gagctggaga gcacctcaga gaccagtgac 720
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gcctga                                                            1026
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<210> 32
<211> 341
<212> PRT
<213> Homo sapiens

<400> 32

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Met Leu Leu Leu Val Ala Gln Arg Asp Arg Ala Ser Arg Ile Phe Pro
  1               5                  10                  15

His Leu Tyr Leu Gly Ser Glu Trp Asn Ala Ala Asn Leu Glu Glu Leu
             20                  25                  30

Gln Arg Asn Arg Val Thr His Ile Leu Asn Met Ala Arg Glu Ile Asp
         35                  40                  45

Asn Phe Tyr Pro Glu Arg Phe Thr Tyr His Asn Val Arg Leu Trp Asp
     50                  55                  60

Glu Glu Ser Ala Gln Leu Leu Pro His Trp Lys Glu Thr His Arg Phe
 65                  70                  75                  80

Ile Glu Ala Ala Arg Ala Gln Gly Thr His Val Leu Val His Cys Lys
                 85                  90                  95

Met Gly Val Ser Arg Ser Ala Ala Thr Val Leu Ala Tyr Ala Met Lys
            100                 105                 110

Gln Tyr Glu Cys Ser Leu Glu Gln Ala Leu Arg His Val Gln Glu Leu
        115                 120                 125

Arg Pro Ile Ala Arg Pro Asn Pro Gly Phe Leu Arg Gln Leu Gln Ile
    130                 135                 140

Tyr Gln Gly Ile Leu Thr Ala Ser Arg Gln Ser His Val Trp Glu Gln
145                 150                 155                 160

Lys Val Gly Gly Val Ser Pro Glu Glu His Pro Ala Pro Glu Val Ser
                165                 170                 175

Thr Pro Phe Pro Pro Leu Pro Pro Glu Pro Glu Gly Gly Gly Glu Glu
            180                 185                 190

Lys Val Val Gly Met Glu Glu Ser Gln Ala Ala Pro Lys Glu Glu Pro
        195                 200                 205
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Gly Pro Arg Pro Arg Ile Asn Leu Arg Gly Val Met Arg Ser Ile Ser
    210                 215                 220

Leu Leu Glu Pro Ser Leu Glu Leu Glu Ser Thr Ser Glu Thr Ser Asp
225                 230                 235                 240

Met Pro Glu Val Phe Ser Ser His Glu Ser Ser His Glu Glu Pro Leu
                245                 250                 255

Gln Pro Phe Pro Gln Leu Ala Arg Thr Lys Gly Gly Gln Gln Val Asp
            260                 265                 270

Arg Gly Pro Gln Pro Ala Leu Lys Ser Arg Gln Ser Val Val Thr Leu
        275                 280                 285

Gln Gly Ser Ala Val Val Ala Asn Arg Thr Gln Ala Phe Gln Glu Gln
    290                 295                 300

Glu Gln Gly Gln Gly Gln Gly Gln Gly Glu Pro Cys Ile Ser Ser Thr
305                 310                 315                 320

Pro Arg Phe Arg Lys Val Val Arg Gln Ala Ser Val His Asp Ser Gly
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Glu Glu Gly Glu Ala
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<210> 33
<211> 3995
<212> DNA
<213> Homo sapiens

<400> 33

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<210> 34
<211> 777
<212> PRT
<213> Homo sapiens

<400> 34
Met Phe Ser Leu Lys Pro Pro Lys Pro Thr Phe Arg Ser Tyr Phe Leu
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Pro Pro Pro Gln Thr Asp Asp Lys Ile Asn Ser Glu Pro Lys Ile Lys
20 25 30

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Lys Leu Glu Pro Val Leu Leu Pro Gly Glu Ile Val Val Asn Glu Val
          35                  40                  45

Asn Phe Val Arg Lys Cys Ile Ala Thr Asp Thr Ser Gln Tyr Asp Leu
      50                  55                  60

Trp Gly Lys Leu Ile Cys Ser Asn Phe Lys Ile Ser Phe Ile Thr Asp
 65                  70                  75                  80

Asp Pro Met Pro Leu Gln Lys Phe His Tyr Arg Asn Leu Leu Leu Gly
                 85                  90                  95

Glu His Asp Val Pro Leu Thr Cys Ile Glu Gln Ile Val Thr Val Asn
            100                 105                 110

Asp His Lys Arg Lys Gln Lys Val Leu Gly Pro Asn Gln Lys Leu Lys
        115                 120                 125

Phe Asn Pro Thr Glu Leu Ile Ile Tyr Cys Lys Asp Phe Arg Ile Val
    130                 135                 140

Arg Phe Arg Phe Asp Glu Ser Gly Pro Glu Ser Ala Lys Lys Val Cys
145                 150                 155                 160

Leu Ala Ile Ala His Tyr Ser Gln Pro Thr Asp Leu Gln Leu Leu Phe
                165                 170                 175

Ala Phe Glu Tyr Val Gly Lys Lys Tyr His Asn Ser Ala Asn Lys Ile
            180                 185                 190

Asn Gly Ile Pro Ser Gly Asp Gly Gly Gly Gly Gly Gly Gly Gly Asn
        195                 200                 205

Gly Ala Gly Gly Gly Ser Ser Gln Lys Thr Pro Leu Phe Glu Thr Tyr
    210                 215                 220

Ser Asp Trp Asp Arg Glu Ile Lys Arg Thr Gly Ala Ser Gly Trp Arg
225                 230                 235                 240

Val Cys Ser Ile Asn Glu Gly Tyr Met Ile Ser Thr Cys Leu Pro Glu
                245                 250                 255

Tyr Ile Val Val Pro Ser Ser Leu Ala Asp Gln Asp Leu Lys Ile Phe
            260                 265                 270

Ser His Ser Phe Val Gly Arg Arg Met Pro Leu Trp Cys Trp Ser His
        275                 280                 285

Ser Asn Gly Ser Ala Leu Val Arg Met Ala Leu Ile Lys Asp Val Leu
    290                 295                 300

Gln Gln Arg Lys Ile Asp Gln Arg Ile Cys Asn Ala Ile Thr Lys Ser
305                 310                 315                 320

His Pro Gln Arg Ser Asp Val Tyr Lys Ser Asp Leu Asp Lys Thr Leu
                325                 330                 335
```

```
Pro Asn Ile Gln Glu Val Gln Ala Ala Phe Val Lys Leu Lys Gln Leu
            340                 345                 350

Cys Val Asn Glu Pro Phe Glu Glu Thr Glu Glu Lys Trp Leu Ser Ser
        355                 360                 365

Leu Glu Asn Thr Arg Trp Leu Glu Tyr Val Arg Ala Phe Leu Lys His
    370                 375                 380

Ser Ala Glu Leu Val Tyr Met Leu Glu Ser Lys His Leu Ser Val Val
385                 390                 395                 400

Leu Gln Glu Glu Glu Gly Arg Asp Leu Ser Cys Cys Val Ala Ser Leu
                405                 410                 415

Val Gln Val Met Leu Asp Pro Tyr Phe Arg Thr Ile Thr Gly Phe Gln
            420                 425                 430

Ser Leu Ile Gln Lys Glu Trp Val Met Ala Gly Tyr Gln Phe Leu Asp
        435                 440                 445

Arg Cys Asn His Leu Lys Arg Ser Glu Lys Glu Ser Pro Leu Phe Leu
    450                 455                 460

Leu Phe Leu Asp Ala Thr Trp Gln Leu Leu Glu Gln Tyr Pro Ala Ala
465                 470                 475                 480

Phe Glu Phe Ser Glu Thr Tyr Leu Ala Val Leu Tyr Asp Ser Thr Arg
                485                 490                 495

Ile Ser Leu Phe Gly Thr Phe Leu Phe Asn Ser Pro His Gln Arg Val
            500                 505                 510

Lys Gln Ser Thr Glu Phe Ala Ile Ser Lys Asn Ile Gln Leu Gly Asp
        515                 520                 525

Glu Lys Gly Leu Lys Phe Pro Ser Val Trp Asp Trp Ser Leu Gln Phe
    530                 535                 540

Thr Ala Lys Asp Arg Thr Leu Phe His Asn Pro Phe Tyr Ile Gly Lys
545                 550                 555                 560

Ser Thr Pro Cys Ile Gln Asn Gly Ser Val Lys Ser Phe Lys Arg Thr
                565                 570                 575

Lys Lys Ser Tyr Ser Ser Thr Leu Arg Gly Met Pro Ser Ala Leu Lys
            580                 585                 590

Asn Gly Ile Ile Ser Asp Gln Glu Leu Leu Pro Arg Arg Asn Ser Leu
        595                 600                 605

Ile Leu Lys Pro Lys Pro Asp Pro Ala Gln Gln Thr Asp Ser Gln Asn
    610                 615                 620

Ser Asp Thr Glu Gln Tyr Phe Arg Glu Trp Phe Ser Lys Pro Ala Asn
625                 630                 635                 640
```

```
Leu His Gly Val Ile Leu Pro Arg Val Ser Gly Thr His Ile Lys Leu
                645                 650                 655

Trp Lys Leu Cys Tyr Phe Arg Trp Val Pro Glu Ala Gln Ile Ser Leu
            660                 665                 670

Gly Gly Ser Ile Thr Ala Phe His Lys Leu Ser Leu Leu Ala Asp Glu
        675                 680                 685

Val Asp Val Leu Ser Arg Met Leu Arg Gln Gln Arg Ser Gly Pro Leu
    690                 695                 700

Glu Ala Cys Tyr Gly Glu Leu Gly Gln Ser Arg Met Tyr Phe Asn Ala
705                 710                 715                 720

Ser Gly Pro His His Thr Asp Thr Ser Gly Thr Pro Glu Phe Leu Ser
                725                 730                 735

Ser Ser Phe Pro Phe Ser Pro Val Gly Asn Leu Cys Arg Arg Ser Ile
            740                 745                 750

Leu Gly Thr Pro Leu Ser Lys Phe Leu Ser Gly Ala Lys Ile Trp Leu
        755                 760                 765

Ser Thr Glu Thr Leu Ala Asn Glu Asp
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<210> 35
<211> 2353
<212> DNA
<213> Homo sapiens

<400> 35

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<210> 36
<211> 629
<212> PRT
<213> Homo sapiens

<400> 36

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Met Val Pro Pro Lys Leu Gln Glu Ala Phe Glu Pro Phe Asp Leu Lys
  1               5                  10                  15

His Ala Gly Ala His Phe Arg Ala Pro Pro Arg Glu Ser Leu Asp His
             20                  25                  30

Arg Glu Asn Arg Val Phe Arg Gly Phe Ala Pro Pro Asp Lys Arg Asn
         35                  40                  45

Glu Gln Ala Gly Ser Ser Ser Ala Val Val Ser Val Phe Tyr Val Cys
     50                  55                  60

Gly Met Ala Gln Tyr Ser Ser Ser Ser Ser Ser Val Ala Gln Gly Ser
 65                  70                  75                  80

Arg Lys Val Glu Asn Val Arg Leu Val Asp Arg Val Ser Pro Lys Lys
                 85                  90                  95

Ala Ala Leu Gly Thr Leu Tyr Leu Thr Ala Thr His Val Ile Phe Val
            100                 105                 110

Glu Asn Ser Pro Asp Ala Arg Lys Glu Thr Trp Ile Leu His Ser Gln
        115                 120                 125

Ile Ser Thr Ile Glu Lys Gln Ala Thr Thr Ala Thr Gly Cys Pro Leu
    130                 135                 140

Leu Ile Arg Cys Lys Asn Phe Gln Ile Ile Gln Leu Ile Ile Pro Gln
145                 150                 155                 160

Glu Arg Asp Cys His Asp Val Tyr Ile Ser Leu Ile Arg Leu Ala Arg
                165                 170                 175
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Pro Val Lys Tyr Glu Glu Leu Tyr Cys Phe Ser Phe Asn Pro Met Leu
            180                 185                 190

Asp Lys Glu Glu Arg Glu Gln Gly Trp Val Leu Ile Asp Leu Ser Glu
        195                 200                 205

Glu Tyr Thr Arg Met Gly Leu Pro Asn His Tyr Trp Gln Leu Ser Asp
    210                 215                 220

Val Asn Arg Asp Tyr Arg Val Cys Asp Ser Tyr Pro Thr Glu Leu Tyr
225                 230                 235                 240

Val Pro Lys Ser Ala Thr Ala His Ile Ile Val Gly Ser Ser Lys Phe
                245                 250                 255

Arg Ser Arg Arg Arg Phe Pro Val Leu Ser Tyr Tyr Tyr Lys Asp Asn
            260                 265                 270

His Ala Ser Ile Cys Arg Ser Ser Gln Pro Leu Ser Gly Phe Ser Ala
        275                 280                 285

Arg Cys Leu Glu Asp Glu Gln Met Leu Gln Ala Ile Arg Lys Ala Asn
    290                 295                 300

Pro Gly Ser Asp Phe Val Tyr Val Val Asp Thr Arg Pro Lys Leu Asn
305                 310                 315                 320

Ala Met Ala Asn Arg Ala Ala Gly Lys Gly Tyr Glu Asn Glu Asp Asn
                325                 330                 335

Tyr Ser Asn Ile Lys Phe Gln Phe Ile Gly Ile Glu Asn Ile His Val
            340                 345                 350

Met Arg Asn Ser Leu Gln Lys Met Leu Glu Val Cys Glu Leu Lys Ser
        355                 360                 365

Pro Ser Met Ser Asp Phe Leu Trp Gly Leu Glu Asn Ser Gly Trp Leu
    370                 375                 380

Arg His Ile Lys Ala Ile Met Asp Ala Gly Ile Phe Ile Ala Lys Ala
385                 390                 395                 400

Val Ser Glu Glu Gly Ala Ser Val Leu Val His Cys Ser Asp Gly Trp
                405                 410                 415

Asp Arg Thr Ala Gln Val Cys Ser Val Ala Ser Leu Leu Leu Asp Pro
            420                 425                 430

His Tyr Arg Thr Leu Lys Gly Phe Met Val Leu Ile Glu Lys Asp Trp
        435                 440                 445

Ile Ser Phe Gly His Lys Phe Asn His Arg Tyr Gly Asn Leu Asp Gly
    450                 455                 460

Asp Pro Lys Glu Ile Ser Pro Val Ile Asp Gln Phe Ile Glu Cys Val
465                 470                 475                 480
```

```
Trp Gln Leu Met Glu Gln Phe Pro Cys Ala Phe Glu Phe Asn Glu Arg
                485                 490                 495

Phe Leu Ile His Ile Gln His His Ile Tyr Ser Cys Gln Phe Gly Asn
            500                 505                 510

Phe Leu Cys Asn Ser Gln Lys Glu Arg Arg Glu Leu Lys Ile Gln Glu
        515                 520                 525

Arg Thr Tyr Ser Leu Trp Ala His Leu Trp Lys Asn Arg Ala Asp Tyr
    530                 535                 540

Leu Asn Pro Leu Phe Arg Ala Asp His Ser Gln Thr Gln Gly Thr Phe
545                 550                 555                 560

His Leu Pro Thr Thr Pro Cys Asn Phe Met Tyr Lys Phe Trp Ser Gly
                565                 570                 575

Met Tyr Asn Arg Phe Glu Lys Gly Met Gln Pro Arg Gln Ser Val Thr
            580                 585                 590

Asp Tyr Leu Met Ala Val Lys Glu Glu Thr Gln Gln Leu Glu Glu Glu
        595                 600                 605

Leu Glu Ala Leu Glu Glu Val Arg His Thr Cys Phe Val Asn Leu Phe
    610                 615                 620

Ser Val Leu Ile Ser
625
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<210> 37
<211> 1200
<212> DNA
<213> Homo sapiens

<400> 37

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gacagtccac agacaaacga atttaaagga gcaaccgagg aggcacctgc gaaagaaagc 120
ccacacacaa gtgaatttaa aggagcagcc ctggtgtcac ctatcagtaa aagtatgtta 180
gaacgacttt ccaagtttga agttgaagat gctgaaaatg ttgcttcata tgacagcaag 240
attaagaaaa ttgtgcattc aattgtatca tcctttgcat ttggactatt tggagttttc 300
ctggtcttac tggatgtcac tctcgtcctt gccgacctaa ttttcactga cagcaaactt 360
tatattcctt cggagtatcg ttctatttct ctagctattg ccttatttct tctcatggat 420
gttcttcttc gagtatttgt agaagggccc gtctatacca ttgggctgcc cccttcagac 480
ctccgggcag gaaaagaaga gactgtactg gtcagagaaa gacatcagca ggagagccag 540
agattcctcc tcctctccat catcaccatc accattattc tcatcaccat caccgtcacc 600
gtcatcaaat attttaattt aactaaaaat attaaacttg aaatcagtaa gatggtggta 660
ttctccaagg aagtaaatga gtggatgact caagatcctg aaaacatcat agtgattcac 720
tgtaaaggag gcaaaatcat catcaccatc atggacttca aagaagtttg tacaactcaa 780
tattgcaaag ttgtcagttc tctcaagtta atctataaat tcaatgtagt tccaataaaa 840
atcctaaatg tgaaaggaag aaccggaact atggtttgtg cgctccttat tgcctccgaa 900
atatttttaa ctgcagagga aagcctgtat tattttggag aaaggcgaac agataaaacc 960
cacagcaata aatttcaggg agtagaaact ccttgtcaga atagatatgt tggatatttt 1020
gcacaagtga aacatctcta caacgggaat atccctccaa gacggatact ctttataaaa 1080
agattcatta tttattcgac tcgtggtgtt ggaacaggtg atgtatgtga tctacaattc 1140
caaatagtaa tggagaaaaa ggttgtcttt tccagtactt cattaggaaa ttgttcgctg 1200
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<210> 38
<211> 400
<212> PRT
<213> Homo sapiens

<400> 38

```
Met Asn Glu Ser Pro Asp Pro Asn Ala Leu Ala Gly Val Ile Ile Glu
  1               5                  10                  15

Arg Ala Pro Ser Asp Ser Pro Gln Thr Asn Glu Phe Lys Gly Ala Thr
             20                  25                  30

Glu Glu Ala Pro Ala Lys Glu Ser Pro His Thr Ser Glu Phe Lys Gly
         35                  40                  45

Ala Ala Leu Val Ser Pro Ile Ser Lys Ser Met Leu Glu Arg Leu Ser
     50                  55                  60

Lys Phe Glu Val Glu Asp Ala Glu Asn Val Ala Ser Tyr Asp Ser Lys
 65                  70                  75                  80

Ile Lys Lys Ile Val His Ser Ile Val Ser Ser Phe Ala Phe Gly Leu
                 85                  90                  95

Phe Gly Val Phe Leu Val Leu Leu Asp Val Thr Leu Val Leu Ala Asp
            100                 105                 110

Leu Ile Phe Thr Asp Ser Lys Leu Tyr Ile Pro Ser Glu Tyr Arg Ser
        115                 120                 125

Ile Ser Leu Ala Ile Ala Leu Phe Phe Leu Met Asp Val Leu Leu Arg
    130                 135                 140

Val Phe Val Glu Gly Pro Val Tyr Thr Ile Gly Leu Pro Pro Ser Asp
145                 150                 155                 160

Leu Arg Ala Gly Lys Glu Glu Thr Val Leu Val Arg Glu Arg His Gln
                165                 170                 175

Gln Glu Ser Gln Arg Phe Leu Leu Leu Ser Ile Ile Thr Ile Thr Ile
            180                 185                 190

Ile Leu Ile Thr Ile Thr Val Thr Val Ile Lys Tyr Phe Asn Leu Thr
        195                 200                 205

Lys Asn Ile Lys Leu Glu Ile Ser Lys Met Val Val Phe Ser Lys Glu
    210                 215                 220

Val Asn Glu Trp Met Thr Gln Asp Pro Glu Asn Ile Ile Val Ile His
225                 230                 235                 240

Cys Lys Gly Gly Lys Ile Ile Ile Thr Ile Met Asp Phe Lys Glu Val
                245                 250                 255

Cys Thr Thr Gln Tyr Cys Lys Val Val Ser Ser Leu Lys Leu Ile Tyr
            260                 265                 270
```

```
Lys Phe Asn Val Val Pro Ile Lys Ile Leu Asn Val Lys Gly Arg Thr
        275                 280                 285

Gly Thr Met Val Cys Ala Leu Leu Ile Ala Ser Glu Ile Phe Leu Thr
    290                 295                 300

Ala Glu Glu Ser Leu Tyr Tyr Phe Gly Glu Arg Arg Thr Asp Lys Thr
305                 310                 315                 320

His Ser Asn Lys Phe Gln Gly Val Glu Thr Pro Cys Gln Asn Arg Tyr
                325                 330                 335

Val Gly Tyr Phe Ala Gln Val Lys His Leu Tyr Asn Gly Asn Ile Pro
            340                 345                 350

Pro Arg Arg Ile Leu Phe Ile Lys Arg Phe Ile Ile Tyr Ser Thr Arg
        355                 360                 365

Gly Val Gly Thr Gly Asp Val Cys Asp Leu Gln Phe Gln Ile Val Met
    370                 375                 380

Glu Lys Lys Val Val Phe Ser Ser Thr Ser Leu Gly Asn Cys Ser Leu
385                 390                 395                 400
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<210> 39
<211> 694
<212> DNA
<213> Homo sapiens

<400> 39

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gttcctgttg gacctgggcg tgcggcacct ggtgtccctg acggagcgcg ggccccctca 180
cagcgacagc tgccccggcc tcaccctgca ccgcctgcgc atccccgact tctgcccgcc 240
ggcccccgac cagatcgacc gcttcgtgca gatcgtggac gaggccaacg cacggggaga 300
ggctgtggga gtgcactgtg ctctgggctt tggccgcact ggcaccatgc tggcctgtta 360
cctggtgaag gagcggggct tggctgcagg agatgccatt gctgaaatcc gacgactacg 420
acccggcccc atcgagacct atgagcagga gaaagcagtc ttccagttct accagcgaac 480
gaaataaggg gccttagtac ccttctacca ggccctcact ccccttcccc atgttgtcga 540
tggggccaga gatgaaggga agtggactaa agtattaaac cctctagctc ccattggctg 600
aagacactga agtagcccac ccctgcaggc aggtcctgat tgaaggggag gcttgtactg 660
ctttgttgaa taaatgagtt ttacgaacca ggga                          694
```

<210> 40
<211> 150
<212> PRT
<213> Homo sapiens

<400> 40

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Met Gly Val Gln Pro Pro Asn Phe Ser Trp Val Leu Pro Gly Arg Leu
  1               5                  10                  15

Ala Gly Leu Ala Leu Pro Arg Leu Pro Ala His Tyr Gln Phe Leu Leu
             20                  25                  30
```

```
Asp Leu Gly Val Arg His Leu Val Ser Leu Thr Glu Arg Gly Pro Pro
         35                  40                  45

His Ser Asp Ser Cys Pro Gly Leu Thr Leu His Arg Leu Arg Ile Pro
     50                  55                  60

Asp Phe Cys Pro Pro Ala Pro Asp Gln Ile Asp Arg Phe Val Gln Ile
 65                  70                  75                  80

Val Asp Glu Ala Asn Ala Arg Gly Glu Ala Val Gly Val His Cys Ala
                 85                  90                  95

Leu Gly Phe Gly Arg Thr Gly Thr Met Leu Ala Cys Tyr Leu Val Lys
            100                 105                 110

Glu Arg Gly Leu Ala Ala Gly Asp Ala Ile Ala Glu Ile Arg Arg Leu
        115                 120                 125

Arg Pro Gly Pro Ile Glu Thr Tyr Glu Gln Glu Lys Ala Val Phe Gln
    130                 135                 140

Phe Tyr Gln Arg Thr Lys
145                 150
```

<210> 41
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<220>
<221> modified_base
<222> (57)
<223> a, c, g, t, other or unknown

<400> 41
aagcagtggt aacaacgcag agtacttttt ttttttttt ttttttttt tttttvn 57

<210> 42
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 42
aagtggcaac agagataacg cgtacgcggg 30

<210> 43
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 43
aagcagtggt aacaacgcag agtacgcggg 30

<210> 44
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 44
aagcagtggt aacaacgcag agt 23

<210> 45
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 45
aagtggcaac agagataacg cgt 23